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     (FILE 'HOME' ENTERED AT 07:55:58 ON 10 MAR 2003)

     INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
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                1   FILE ADISINSIGHT
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               55   FILE ANABSTR
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             1423   FILE BIOSIS
              296   FILE BIOTECHABS
              296   FILE BIOTECHDS
              531   FILE BIOTECHNO
              221   FILE CABA
               78   FILE CANCERLIT
             2051   FILE CAPLUS
               53   FILE CEABA-VTB
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               49   FILE CONFSCI
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               61   FILE DDFB
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               61   FILE DRUGB
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              858   FILE EMBASE
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               24   FILE FEDRIP
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             2344   FILE GENBANK
               76   FILE IFIPAT
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              436   FILE LIFESCI
             2321   FILE MEDLINE
                1   FILE NIOSHTIC
               12   FILE NTIS
                8   FILE OCEAN
              335   FILE PASCAL
                2   FILE PHAR
                2   FILE PHIN
               10   FILE PROMT
              984   FILE SCISEARCH
              512   FILE TOXCENTER
              470   FILE USPATFULL
                3   FILE USPAT2
                2   FILE VETB
               10   FILE VETU
              139   FILE WPIDS
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     ENTERED AT 07:57:19 ON 10 MAR 2003
L2             31 S L1 AND SYNECHOCYSTIS
L3             11 DUP REM L2 (20 DUPLICATES REMOVED)
L4            137 S L1 AND PIG
L5             24 S L4 AND (CDNA OR CLON?)
L6             12 DUP REM L5 (12 DUPLICATES REMOVED)
L7              1 S L6 AND SYNECHOCYSTIS
L8              1 S L4 AND SYNECHOCYSTIS

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L3 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
ACCESSION NUMBER: 2002:171290 CAPLUS
DOCUMENT NUMBER: 136:385015
TITLE: Production of N-acetyl-D-neuraminic acid by coupling bacteria expressing N-acetyl-D-glucosamine 2-**epimerase** and N-acetyl-D-neuraminic acid synthetase
AUTHOR(S): Tabata, Kazuhiko; Koizumi, Satoshi; Endo, Tetsuo; Ozaki, Akio
CORPORATE SOURCE: Kyowa Hakko Kogyo Co., Ltd., Tokyo Research Laboratories, Tokyo, Machida, 194-8533, Japan
SOURCE: Enzyme and Microbial Technology (2002), 30(3), 327-333
CODEN: EMTED2; ISSN: 0141-0229
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB N-acetyl-D-glucosamine (GlcNAc) 2-**epimerase** catalyzes the interconversion between GlcNAc and N-acetyl-D-mannosamine (ManNAc) that is a precursor of N-acetyl-D-neuraminic acid (NeuAc). Homol. search using the sequence of the porcine GlcNAc 2-**epimerase** as a query revealed that a gene product (Slr1975) of **Synechocystis** sp. PCC6803 showed significant homol. When the gene of slr1975 was cloned by PCR and expressed in Escherichia coli, the recombinant E. coli showed GlcNAc 2-**epimerase** activity. This is the first example of the cloning of the gene for GlcNAc 2-**epimerase** from prokaryotes. GlcNAc 2-**epimerase** was purified from E. coli overexpressing slr1975, and the enzymic properties were detd. Mol. wt. by SDS-PAGE was 45 kDa, similar to that predicted by the sequence. Km values for GlcNAc and ManNAc were 6.94 mM and 4.76 mM, resp., and ATP was essential for the activity. Microbial prodn. of NeuAc was carried out using E. coli cells overexpressing GlcNAc 2-**epimerase** and NeuAc synthetase as enzyme sources. Phosphoenolpyruvate and ATP, required as a substrate or a cofactor of the enzymes, were supplied by the activities of E. coli and Corynebacterium ammoniagenes cells. Starting with 800 mM GlcNAc and 360 mM glucose, NeuAc accumulated at 39.7 mM (12.3 g l-1) after 22 h.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:781090 CAPLUS
DOCUMENT NUMBER: 135:328754
TITLE: Crystal structure of Methanobacterium thermoautotrophicum RmlC enzyme, identification of RmlC inhibitors and use for antibacterial drug design
INVENTOR(S): Christendat, Dinesh; Edwards, Aled M.; Pai, Emil F.; Bochkarev, Alexei; Saridakis, Vivian
PATENT ASSIGNEE(S): University Health Network, Can.
SOURCE: PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001079457	A2	20011025	WO 2001-CA512	20010412

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,

RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-196915P P 20000413

AB The invention provides the crystal structure of Methanobacterium thermoautotrophicum dTDP-4-keto-6-deoxy-D-hexulose 3,5-**epimerase** (MT RmlC) in the presence and absence of dTDP, a substrate analog, and identifies the active site of the enzyme. The crystal structure can be used to det. the crystal structure of homologs, analogs, mutants and co-complexes of MT RmlC and to identify and design inhibitors to RmlC. The present invention has applicability in identifying and designing anti-bacterial agents and the treatment of bacterial infections.

L3 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:167696 CAPLUS
DOCUMENT NUMBER: 134:221520
TITLE: Process for producing N-acetylneuraminic acid
INVENTOR(S): Koizumi, Satoshi; Tabata, Kazuhiko; Endo, Tetsuo; Ozaki, Akio
PATENT ASSIGNEE(S): Kyowa Hakko Kogyo Co., Ltd., Japan
SOURCE: Eur. Pat. Appl., 24 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1081230	A2	20010307	EP 2000-118139	20000829
EP 1081230	A3	20020605		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001136982	A2	20010522	JP 2000-257221	20000828
CN 1286308	A	20010307	CN 2000-126405	20000830

PRIORITY APPLN. INFO.: JP 1999-242670 A 19990830
OTHER SOURCE(S): CASREACT 134:221520

AB The present invention provides a process for economically producing N-acetylneuraminic acid without using expensive materials such as pyruvic acid and phosphoenolpyruvic acid. The process is based on contacting microorganisms, which possess N-acetylneuraminic acid aldolase or N-acetylneuraminic acid synthetase activities, and that are capable of producing pyruvic acid or phosphoenolpyruvic acid, with a reaction mixt. contg. N-acetylmannosamine as a precursor and a suitable microbial energy source such as glucose or fructose. The N-acetylmannosamine for this reaction is supplied by the reaction of N-acetylglucosamine with a recombinant microorganism possessing a N-acetylglucosamine 2-**epimerase** activity derived from a **Synechocystis** strain. Microorganisms possessing a N-acetylneuraminic acid aldolase activity may be selected from the genera Escherichia or Corynebacterium. Microorganisms possessing a N-acetylneuraminic acid synthetase activity may be selected from the genera Escherichia, Neisseria or Streptococcus. Microorganisms producing pyruvic or phosphoenolpyruvic acid may be selected from the genera Escherichia, Corynebacterium, or Saccharomyces. The preferred microorganisms form these genera are Escherichia coli, Corynebacterium ammoniagenes, C. glutamicum, or C. acetoacidophilum. Thus, 50 g/L wet cells of Escherichia coli strain NM522/pYP18, which has a N-acetylneuraminic acid synthetase activity, 50 g/L wet cells of E. coli strain NM522/pYP16, which has a N-acetylglucosamine 2-**epimerase** activity, 150 g/L wet cells of C. ammoniagenes, 100 g/L glucose, and 180 g/L N-acetylglucosamine were reacted at 32 .degree.C, pH 7.2 for 22 h. Once the reaction had been completed, 12.3 g/L N-acetylneuraminic acid had

been formed.

L3 ANSWER 4 OF 11 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001187164 MEDLINE
DOCUMENT NUMBER: 21172900 PubMed ID: 11275551
TITLE: Identification of functionally important cysteine residues of the human renin-binding protein as the enzyme N-acetyl-D-glucosamine 2-**epimerase**.
AUTHOR: Takahashi S; Takahashi K; Kaneko T; Ogasawara H; Shindo S; Saito K; Kawamura Y
CORPORATE SOURCE: Department of Bioengineering, Akita Research Institute of Food and Brewing (ARIF), Sanuki, Arayamachi, Akita 010-1623, Japan.. saori@arif.pref.akita.jp
SOURCE: JOURNAL OF BIOCHEMISTRY, (2001 Apr) 129 (4) 529-35. Journal code: 0376600. ISSN: 0021-924X.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20010903
Entered Medline: 20010830

AB Renin-binding protein (RnBP) is an endogenous renin inhibitor originally isolated from porcine kidney. It was recently identified as the enzyme N-acetyl-D-glucosamine (GlcNAc) 2-**epimerase** [Takahashi, S. et al. (1999) J. Biochem. 125, 348-353] and its active site residue was determined to be cysteine 380 by site-directed mutagenesis [Takahashi, S. et al. (1999) J. Biochem. 126, 639-642]. To further investigate the relationship between structure and function of recombinant human (rh) RnBP as a GlcNAc 2-**epimerase**, we have constructed several C-terminal deletion and multi-cysteine/serine mutants of rhGlcNAc 2-**epimerase** and expressed them in Escherichia coli cells. The expression was detected by Western blotting using anti-rhRnBP antiserum. The C-terminal deletion mutant, Delta400-417, had approximately 50% activity relative to the wild-type enzyme, but other C-terminal deletion mutants, Delta380-417, Delta386-417, and Delta390-417, had no enzymatic activity. Mutational analysis of multi-cysteine/serine mutants revealed that cysteines 41 and 390 were critical for the activity or stabilization of the enzyme, while cysteine residues in the middle of the enzyme, cysteines 125, 210, 239, and 302, had no essential function in relation to the activity.

L3 ANSWER 5 OF 11 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:211989 BIOSIS
DOCUMENT NUMBER: PREV200200211989
TITLE: Cloning, sequencing, and expression of galE gene of Bradyrhizobium japonicum: galE knock-out mutant is defective in both LPS synthesis and nodulation of soybean.
AUTHOR(S): Park, K. (1); Chang, C. (1); Lee, S. (1); Noh, J. (1); Koh, S.; So, J. (1)
CORPORATE SOURCE: (1) Inha Univ., Inchon South Korea
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 432. http://www.asmusa.org/mtgsrc/generalmeeting.htm. print. Meeting Info.: 101st General Meeting of the American Society for Microbiology Orlando, FL, USA May 20-24, 2001 ISSN: 1060-2011.
DOCUMENT TYPE: Conference
LANGUAGE: English

AB The enzyme UDP-galactose 4-**epimerase** (GalE) is involved in one of the major steps of galactose metabolism in bacteria. GalE mediates the incorporation of galactose in extracellular polysaccharide materials such as the O-side chain of lipopolysaccharide (LPS). In this study, we describe the cloning and characterization of the galE gene from

Brdayrhizobium japonicum, a soybean endosymbiont. Nucleotide sequence analysis of the cloned DNA identified the galE gene: Comparison of the deduced amino acid sequence with published data showed a significant homology with the GalE of Azospirillum brasilense (68%), Aquifex aeolicus (68%), and **Synechocystis** sp. (66%). Functional identity was achieved by the complementation of a galE mutant strain of Escherichia coli PL2 with the subcloned genes. Galactose **epimerase** activity of the complemented strain was essentially identical to that of the wild type E. coli DH5. In vivo expression study showed that a 36 kDa protein was expressed from the complementing plasmids. To study the role of galE gene in B. japonicum LPS biosynthesis, the galE gene was inactivated in chromosome by double cross-over homologous recombination where galE knock-out fragment replaced the galE gene in B. japonicum. To confirm the inactivation of the galE gene in chromosomal DNA, genomic Southern blot hybridization was performed. A galE knock-out mutant strain of B. japonicum was found to be far more hydrophobic than the wild type strain based on the cell surface hydrophobicity (CSH). SDS-PAGE analysis of LPS from the galE knock-out mutant showed an LPS profile completely devoid of O-antigenic part. A standard plant infection test using the wild type and galE defective B. japonicum strains revealed that the galE gene is indeed involved in nodulation process of B. japonicum with its soybean host plant.

L3 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:573926 CAPLUS
DOCUMENT NUMBER: 133:174002
TITLE: **Synechocystis** N-acetylglucosamine 2-**epimerase**, gene, recombinant expression, and use in N-Acetylmannosamine synthesis
INVENTOR(S): Koizumi, Satoshi; Tabata, Kazuhiko; Endo, Tetsuo; Ozaki, Akio
PATENT ASSIGNEE(S): Kyowa Hakko Kogyo Co., Ltd., Japan
SOURCE: PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000047730	A1	20000817	WO 2000-JP702	20000209
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1154018	A1	20011114	EP 2000-902868	20000209
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: JP 1999-31035 A 19990209
WO 2000-JP702 W 20000209

AB A novel protein having an N-acetylglucosamine 2-**epimerase** activity; a DNA encoding this protein; a recombinant vector contg. this DNA; a transformant obtained by transferring this recombinant vector into a host cell; and a process for producing the above protein or N-Acetylmannosamine by using this transformant, are disclosed. A gene homologous to pig N-acetylglucosamine 2-**epimerase** was identified through database search in **Synechocystis**, and cloned. Accumulation of N-acetylglucosamine and N-Acetylmannosamine was detected

in E. coli transformed with the recombinant expression vector contg. the cloned gene.
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:577176 CAPLUS
DOCUMENT NUMBER: 131:225184
TITLE: Cyano2Dbase updated. Linkage of 234 protein spots to corresponding genes through N-terminal microsequencing
AUTHOR(S): Sazuka, Takashi; Yamaguchi, Minoru; Ohara, Osamu
CORPORATE SOURCE: Laboratory DNA Technology, Kazusa DNA Research Institute, Kisarazu, 292, Japan
SOURCE: Electrophoresis (1999), 20(11), 2160-2171
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The cyanobacterium **Synechocystis** sp. strain PCC6803 is an interesting model organism for proteome study because it is a photosynthetic prokaryote and its genomic sequence has already been detd. at our institute. We thus initiated characterization of this organism from a proteomic viewpoint by exploiting two-dimensional (2-D) gel electrophoresis coupled with N-terminal protein sequencing. In a previous study, we linked 130 protein spots on 2-dimensional gels with the genes that encoded them. As an extension of the previous study, the no. of protein spots linked to their corresponding genes was increased to 227 in this study by sep. analyzing cyanobacterial proteins in four different fractions (sol., insol., thylakoid membrane, and secretory protein fractions). The resultant updated 2-D protein-gene linkage database, named Cyano2Dbase, will serve as an indispensable tool in future cyanobacterial proteomic studies. From the data compiled in the Cyano2Dbase, we can ext. many items of information concerning translation, posttranslational processing including characteristics of cyanobacterial signal sequences and modification of cyanobacterial proteins. The Cyano2Dbase is available to the public through the World Wide Web (http://www.kazusa.or.jp/tech/sazuka/cyano/proteome.html).
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 11 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1998238683 MEDLINE
DOCUMENT NUMBER: 98238683 PubMed ID: 9571197
TITLE: The rfb genes in Azotobacter vinelandii are arranged in a rfbFGC gene cluster: a significant deviation to the arrangement of the rfb genes in Enterobacteriaceae.
AUTHOR: Hausman B S; Williamson J A; Schreiner R P; Pulakat L; Gavini N
CORPORATE SOURCE: Department of Biological Sciences, Bowling Green State University, Ohio 43403, USA.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998 Apr 17) 245 (2) 572-82.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980611
Last Updated on STN: 19980611
Entered Medline: 19980602
AB We report the identification of rfbF and rfbC located adjacent to the previously identified rfbG (Gavini et. al. Biochem. Biophys. Res. Commun. 1997, 240, 153-161) from the non-symbiotic, non-pathogenic soil bacterium

Azotobacter vinelandii. The rfbF open reading frame encodes a putative polypeptide of 256 amino acids. This polypeptide shares a homology of 74% with the RfbF of **Synechocystis** sp. and a 70% homology with the AscA of Yersinia pseudotuberculosis which function as alpha-D-glucose-1-phosphate cytidylyltransferases in the biosynthesis of the O-antigen. The rfbC encodes a putative polypeptide of 186 amino acids. It shows strongest homology to the RfbC of **Synechocystis** sp. (64%) and Salmonella typhimurium (40%). RfbC functions as a dTDP-4-Dehydrorhamnose 3,5-**Epimerase**. The genes identified here have a low G + C content (approximately 56%) as compared to the A. vinelandii chromosome (approximately 63%) which is characteristic of the rfb clusters identified in other bacteria and may be indicative of the acquisition of the rfb genes by interspecific gene transfer. Despite the high level of sequence conservation, the organization of the rfb genes in A. vinelandii deviates from the arrangement of the most thoroughly studied rfb gene clusters of Enterobacteriaceae.

L3 ANSWER 9 OF 11 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 1998342075 MEDLINE
DOCUMENT NUMBER: 98342075 PubMed ID: 9675122
TITLE: Spinach CSP41, an mRNA-binding protein and ribonuclease, is homologous to nucleotide-sugar **epimerases** and hydroxysteroid dehydrogenases.
AUTHOR: Baker M E; Grundy W N; Elkan C P
CORPORATE SOURCE: 0623B, 0114, University of California, San Diego, 9500 Gilman Drive, La Jolla, California, 92093-0623, USA.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998 Jul 20) 248 (2) 250-4.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 19980903
Entered Medline: 19980827
AB Spinach CSP41 is part of a protein complex that binds to the 3' untranslated region (UTR) of petD precursor-mRNA, a chloroplast gene encoding subunit IV of the cytochrome b6/f complex. CSP41 cleaves the 3'-UTR of petD mRNA within the stem-loop structure, suggesting a key role in the control of chloroplast mRNA stability. We discovered that CSP41 is homologous to nucleotide-sugar **epimerases** and hydroxysteroid dehydrogenases while seeking distant homologs of these enzymes with a hidden Markov model-based search of Genpept. This analysis identified **Synechocystis** ORF, Accession 1652543 as a homolog. Subsequent analyses show that spinach CSP41 and Arabidopsis thaliana 2765081 are homologous to the **Synechocystis** ORF. Information from the solved 3D structures of **epimerases** and dehydrogenases and our motif analysis of these enzymes is used to predict domains on CSP41 that are important in binding and metabolism of mRNA. Cyanobacteria are among the earliest life forms, indicating that the divergence from a common ancestor of nucleotide-sugar **epimerases** and an mRNA binding protein with ribonuclease activity was ancient.

L3 ANSWER 10 OF 11 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 1998362424 MEDLINE
DOCUMENT NUMBER: 98362424 PubMed ID: 9697098
TITLE: Sequence analysis of the cupin gene family in **Synechocystis** PCC6803.
AUTHOR: Dunwell J M
CORPORATE SOURCE: Department of Agricultural Botany, School of Plant Sciences, University of Reading, UK.

SOURCE: MICROBIAL AND COMPARATIVE GENOMICS, (1998) 3 (2) 141-8.
Journal code: 9616596. ISSN: 1090-6592.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19981021
Last Updated on STN: 19981021
Entered Medline: 19981009

AB The recently described cupin superfamily of proteins includes the germin and germinlike proteins, of which the cereal oxalate oxidase is the best characterized. This superfamily also includes seed storage proteins, in addition to several microbial enzymes and proteins with unknown function. All these proteins are characterized by the conservation of two central motifs, usually containing two or three histidine residues presumed to be involved with metal binding in the catalytic active site. The present study on the coding regions of **Synechocystis** PCC6803 identifies a previously unknown group of 12 related cupins, each containing the characteristic two-motif signature. This group comprises 11 single-domain proteins, ranging in length from 104 to 289 residues, and includes two phosphomannose isomerases and two **epimerases** involved in cell wall synthesis, a member of the pirin group of nuclear proteins, a possible transcriptional regulator, and a close relative of a cytochrome c551 from Rhodococcus. Additionally, there is a duplicated, two-domain protein that has close similarity to an oxalate decarboxylase from the fungus Collybia velutipes and that is a putative progenitor of the storage proteins of land plants.

L3 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 6
ACCESSION NUMBER: 1997:451161 CAPLUS
DOCUMENT NUMBER: 127:215672
TITLE: Cloning and characterization of the D-tagatose 3-**epimerase** gene from Pseudomonas cichorii ST-24
AUTHOR(S): Ishida, Yutaka; Kamiya, Takanori; Itoh, Hiromichi; Kimura, Yoshio; Izumori, Ken
CORPORATE SOURCE: Dep. Bioresource Sci., Fac. Agric., Kagawa Univ., Kagawa, 761-07, Japan
SOURCE: Journal of Fermentation and Bioengineering (1997), 83(6), 529-534
CODEN: JFBIEX; ISSN: 0922-338X
PUBLISHER: Society for Fermentation and Bioengineering, Japan
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The gene encoding D-tagatose 3-**epimerase** (D-TE) from Pseudomonas cichorii ST-24 was cloned and sequenced. It was found to consist of 873 bp encoding 290 amino acid residues. The mol. wt. of the deduced amino acid sequence of D-TE was detd. to be 32.5 kDa. The deduced amino acid sequence showed no extensive homol. with sequences of other sugar-related **epimerases**, but homol. was obsd. with several hypothetical proteins of prokaryotes, i.e. **Synechocystis** sp., Bacillus subtilis, Haemophilus influenzae, and Escherichia coli. The D-TE gene was expressed in E. coli.